

WHAT WE CLAIM IS:

1. A nucleic acid molecule of a sheep type of *M. paratuberculosis* said molecule comprising SEQ ID NO. 1 or a complement thereof.
2. A probe comprising SEQ ID NO.1 or a complement thereof.
- 5 3. A probe comprising at least 6 contiguous nucleotides selected from nucleotides 1 – 35 of SEQ ID NO. 1 a complement thereof.
4. A probe comprising at least 10-12 contiguous nucleotides selected from nucleotides 1 – 35 of SEQ ID NO. 1 or a complement thereof.
5. A probe comprising at least 20 or more contiguous nucleotides selected
10 from nucleotides 1 – 35 of SEQ ID NO. 1 or a complement thereof.
6. A probe comprising at least 6 contiguous nucleotides selected from nucleotides 230 – 260 of SEQ ID NO. 1 or a complement thereof.
7. A probe comprising at least 10-12 contiguous nucleotides selected from nucleotides 230 – 260 of SEQ ID NO. 1 or a complement thereof.
- 15 8. A probe comprising at least 20 or more contiguous nucleotides selected from nucleotides 230 – 260 of SEQ ID NO. 1 or a complement thereof.
9. The use of a nucleic acid molecule or probe as claimed in any one of claims 1-7 for detecting the presence of sheep types of *M. paratuberculosis*.
- 20 10. The use of SEQ ID NO 2 or, a fragment or complement thereof for detecting the presence of cattle types of *M. paratuberculosis*.

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11. A method of distinguishing between cattle and sheep types of *M. paratuberculosis* comprising the step of comparing differences between the nucleotide sequences of SEQ ID NO. 1 and SEQ ID NO. 2 or complements of said sequences.
- 5 12. A method of detecting the presence of *M. paratuberculosis* in a sample via a nucleic acid amplification technique said method comprising the steps of:
- 10 a) taking a sample from an animal or any other source;
- b) extracting nucleic acids from the sample or culturing mycobacteria from the sample and extracting nucleic acids from the mycobacterial culture;
- c) performing a nucleic acid amplification technique; and
- d) determining the identity of the amplification product.
13. A method as claimed in claim 12 wherein the animals may include cattle, sheep, deer, goats, ferrets, rabbits and humans.
- 15 14. A method as claimed in claim 12 wherein step d) of the method comprises identifying the presence of at least 6 nucleotides of the nucleic acid molecule comprising SEQ ID NO. 1 or a complement thereof.
15. A method as claimed in claim 12 wherein step d) of the method comprises identifying the presence of 10-12 contiguous nucleotides of the nucleic acid molecule comprising SEQ ID NO. 1 or a complement thereof.
- 20 16. A method claimed in claim 12 wherein step d) of the method comprises identifying the presence of at least 15 contiguous nucleotides of the nucleic acid molecule comprising SEQ ID NO. 1 or a complement thereof.

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17. A method as claimed in claim 12 wherein step d) of the method comprises identifying the presence of substantially 20 contiguous nucleotides of the nucleic acid molecule comprising SEQ ID NO. 1 or a complement thereof.
- 5 18. A method as claimed in claim 12 wherein step c) utilizes one oligonucleotide primer complementary to at least 6 contiguous nucleotides of SEQ ID NO. 1 or a complement thereof; and one oligonucleotide primer complementary to at least 6 nucleotides of IS900 or a complement thereof.
- 10 19. A method as claimed in claim 12 step c) utilizes one oligonucleotide primer complementary to 10-12 contiguous nucleotides of SEQ ID NO. 1 or a complement thereof; and one oligonucleotide primer complementary to 10-12 nucleotides of IS900 or a complement thereof.
- 15 20. A method as claimed in claim 12 wherein step c) utilizes one oligonucleotide primer complementary to substantially 15 contiguous nucleotides of SEQ ID NO. 1 or a complement thereof; and one oligonucleotide primer complementary to substantially 15 nucleotides of IS900 or a complement thereof.
- 20 21. A method as claimed in claim 12 wherein step c) utilizes one oligonucleotide primer complementary to substantially 20 contiguous nucleotides of SEQ ID NO. 1 or a complement thereof; and one oligonucleotide primer complementary to substantially 20 nucleotides of IS900 or a complement thereof.
22. A method as claimed in claim 12 wherein step c) of the method comprises identifying the presence of at least 6 contiguous nucleotides of the nucleic acid molecule comprising SEQ ID NO. 2 or a complement thereof.

23. A method as claimed in claim 12 wherein step d) of the method comprises identifying the presence of 10-12 contiguous nucleotides of the nucleic acid molecule comprising SEQ ID NO. 2 or a complement thereof.
24. A method as claimed in claim 12 wherein step d) of the method comprises identifying the presence of at least 15 contiguous nucleotides of the nucleic acid molecule comprising SEQ ID NO. 2 or a complement thereof.
25. A method as claimed in claim 12 wherein step d) of the method comprises identifying the presence of approximately 20 contiguous nucleotides of the nucleic acid molecule comprising SEQ ID NO. 2 or a complement thereof.
26. A method as claimed in claim 12 wherein step c) utilizes one oligonucleotide primer complementary to at least 6 contiguous nucleotides of SEQ ID NO. 2 or a complement thereof; and one oligonucleotide primer complementary to at least 6 nucleotides of IS900 or a complement thereof.
27. A method as claimed in claim 12 wherein step c) utilizes one oligonucleotide primer complementary to 10-12 contiguous nucleotides of SEQ ID NO. 2 or a complement thereof; and one oligonucleotide primer complementary to 10-12 nucleotides of IS900 or a complement thereof.
28. A method as claimed in claim 12 wherein step c) utilizes one oligonucleotide primer complementary to substantially 15 contiguous nucleotides of SEQ ID NO. 2 or a complement thereof; and one oligonucleotide primer complementary to substantially 15 nucleotides of IS900 or a complement thereof.
29. A method as claimed in claim 12 wherein step c) utilizes one oligonucleotide primer complementary to substantially 20 contiguous nucleotides of SEQ ID NO. 2 or a complement thereof; and one

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oligonucleotide primer complementary to substantially 20 contiguous nucleotides of IS900 or a complement thereof.

30. The use of a probe comprising at least 6 contiguous nucleotides selected from the nucleic acid comprising SEQ ID NO. 2 or a complement thereof.
- 5 31. The use of a probe comprising substantially 10-12 contiguous nucleotides selected from the nucleic acid comprising SEQ ID NO. 2 or a complement thereof.
32. The use of a probe comprising at least 15 contiguous nucleotides selected from the nucleic acid comprising SEQ ID NO. 2 or a complement thereof.
- 10 33. The use of a probe comprising at least 20 contiguous nucleotides selected from the nucleic acid comprising SEQ ID NO. 2 or a complement thereof.
34. The use of SEQ ID NO.1 and/or SEQ ID NO. 2, or a fragment or complement thereof, to determine whether a strain of either a sheep type or a cattle type of *M. paratuberculosis* is present in a sample.
- 15 35. The use of SEQ ID NO.1, or a fragment or complement thereof, to distinguish any strain of *M. paratuberculosis* from any other strain of the MAI complex which may be present in a sample.
36. The use of SEQ ID NO.2, or a fragment or complement thereof, to distinguish any strain of *M. paratuberculosis* from any other strain of the
- 20 MAI complex which may be present in a sample.
37. The use of SEQ ID NO.1, or a fragment or complement thereof, to distinguish any strain of *M. paratuberculosis* from any strain of the *M. tuberculosis* complex which may be present in a sample.

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38. The use of SEQ ID NO.2, or a fragment or complement thereof, to distinguish any strain of *M. paratuberculosis* from any strain of the *M. tuberculosis* complex which may be present in a sample.
- 5 39. The use of SEQ ID NO. 1, or a fragment or complement thereof, to detect the presence of *M. paratuberculosis* as a causative agent of Johne's disease or Crohn's disease.
40. The use of SEQ ID NO. 2, or a fragment or complement thereof, to detect the presence of *M. paratuberculosis* as a causative agent of Johne's disease or Crohn's disease.

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